

EXPRESS MAIL CERTIFICATE

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. § 1.10 on the date indicated below and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Typed or Printed Name	Margaret Pierce <i>M. Pierce</i>	Express Mail No.	EL 563 388 228 US
Signature		Date	December 29, 2000
NOTIFICATION OF PRIOR SEQUENCE LISTING		Attorney Docket	IRVN-007CON2
		First Named Inventor	Gatanaga, et al.
		Application Number	Unassigned
		Filing Date	Herewith (December 29, 2000)
		Group Art Unit	Unassigned
		Examiner Name	Unassigned
		Title	"FACTORS AFFECTING TUMOR NECROSIS FACTOR RECEPTOR RELEASING ENZYME ACTIVITY"

Sir:

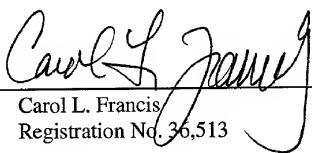
The above-identified patent application contains sequences of nucleic acid and polypeptides. A sequence listing was prepared for the parent application, Application No. PCT/US99/10793, filed May 14, 1999, in paper and computer-readable format. The sequences in the present application are identical to those presented in the parent application. Therefore, please transfer to this application, in accordance with 37 CFR §1.821(e), the computer readable copy from applicants' other application.

As required by 37 CFR §1.821(f), the information in the hard copy and computer readable form are identical. I hereby state that this submission, filed in accordance with 37 CFR §1.821(g), does not contain new material. Applicants respectfully submit that the present patent application is now in compliance with 37 CFR §§1.821-1.825.

The Commissioner is hereby authorized to charge any fees which may be required by this paper, or to credit any overpayment, to Deposit Account No. 50-0815.

Respectfully submitted,
BOZICEVIC, FIELD & FRANCIS LLP

By:


Carol L. Francis
Registration No. 36,513

Date: December 29, 2000

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gatanaga, T.
Granger, G.A.

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USN 09/081,385
(B) FILING DATE: 014-NOV-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTTTTG CTTCTTCC CGGGAAAGG CGGGCCAG AGACCCGCAC TCGGACCAAG	60
CGGGGGCTGC GGGGCCAGAG TGGGCTGGGA AGGCTGGGA GGCGCTCTGG GGCGGGCTCC	120
TCCAGGCTGC GGGCGGCCAG CTCCGGGAAG GCAGTCTGG CCTGGGATG GGCGGGCGG	180
TGGGGCCCGG CGGGCGCGCC TCAGGGAGCC TCAAGCTGC GGAGACGGGA GGAGCGGGCG	240
TGGGGCCCGC AGCGCCGTGG GTGGAGGTGC CGCTGCCCTTC TGAGGGCGAG CCAGTCGGT	300
TGGGACCGG GAGCAGAGCC CGCGCTCTCC CAGCGGCCTC CCGGGGGTC TCACCGGGTC	360
ACCCGAGAGC GGAGGGCCCG GCTCCGAGAG GAGGGGGGC GGCCCCGGGG AAGCAGGCC	420
CTCAGGCGTC GGAGGAGCCC CGAGAAGGAG CTGGGGCTT CCGGGGGGC TCCGACCGCC	480
TGGGTTCCGT CGGGGAGGCC CGAGGCGGCC AGGACCCCA AGGGCAGCTC AGTCAGGGG	540
GCACGACCCA GAGGGCAGCA GAGGAGAGC GGGGGGGGGC CGGGAGAGG CGGGGAGGCC	600
GCTCTGGGA GTTCAAGGCC AGGGCTAGAC TTCAAGGGTC ATGGCTTGC CCCTCATCCC	660
CAGGGAGGTG AGGGGGCTCT GTGAGGAGAG GGGGGGGGG TGAGGAAGGC GTCGCTAGCC	720

AGGGGCGGGG CAGGGGCCA	GGTGGGACT	TAAGGGTGC	TGAAGGGACC	CTCAGGCTGC	780	
AGGGATAGGG AGGGAACTA	GGGGTGTGC	TTGGGGAGGT	GCTGGGGAC	CCGGGGCGCC	840	
CTTTATCTG AAGCCGAATG	TGCTGCCGG	GTCCCCCAGT	ACCTAGAAAT	CCATTCAAG	900	
ATTTCAGGA GTTCAAGGT	GAGACAAGG	CCAGGCCCG	GTGAGAAATG	GGCATGACA	960	
GAGTATGGG TGAGAACCC	GGAGAGAGGA	AGTCCCCGAG	GCGGATGATG	GGACAGAGAG	1020	
CGGGGACCC	AATTTTTAA	AACGCATCTG	AGATCGTTT	GGCACGACTA	1080	
CCTTCACGG AGAAAATGTG	GGCACAGGCC	AGCTCTAAAG	CCAGGCTGC	CCAGCCTGCA	1140	
CTGGCACAGC	TGACGGAAGG	CCAGGGCAGA	GCTTCCCCTC	CTGTCACAG	ACATGAGCCC	1200
TGGAGATCTG GAATGAGGC	GATGTCCTA	GGGAAAGCTG	ATCCGGCCCG	ACCCAGGGCC	1260	
CCCCGGGTG	CCCTTGTG	TGCAATTCTG	TGCGCTCCCTG	CTATCGAAC	1320	
CGGGACCCG	GTGCGTGTG	GCACCTGCA	TGTCAGGAC	CGAACCCAC	1380	
GAGGTGATG	CTGCCCTCCA	GGGGCCTGCC	TGGCTGACAC	TTGCTATGCC	1440	
GAGGGATTGA	GTGGAGCTGC	CGGGCTATCG	GGTGCCTCTG	CTGAGGCGAG	1500	
GCCCCGGTGG	GGTAGGAAAGC	GGCAGGAGAC	AGGTTCCCTG	CAGTCACGG	1560	
GGTCTCATG	CCTAGGAAAC	TGACGGGGGG	TTATGAAAC	GCAGGTGGCT	1620	
CATGGGTTG	CTCTTCAGG	AGGTCTGGT	GGGGGGGGAG	ACTGTACCCC	1680	
CCAGGTGAGG	CGGATGTGGC	CTGGCGCTGT	TGTCCTCTG	ACCTAGTCTT	1740	
CTGGCGCCCA	GGGGCTGGG	GTGACGACAG	TGIGACCGAG	TACCCCGTT	1800	
GTGGGGACAT	TACATCTTC	TAGCTGGAA	CCACAGGCC	GCAGGGTTG	1860	
TCCTCTCCA	TGTTCTCTC	TGAGAACAT	TTACAGGTA	TGTCAGGAG	1920	
CAGGGGAGCT	CAAGTGGAAA	GCCTCTATCC	TTGTCCTCCA	GGAGACAGGA	1980	
TTACAATTC	AGGGACAAGA	CGGTGCACTG	TGAGGTGGG	CAAATCTCAC	2040	
GAGAAATCTG	AGACAGCTTG	CTGGAGGGAC	TGACACCTTG	ACAGGCTCT	2100	
AAGCGATG	GAGAACCCAA	CTGGAGGGAA	CCACATCTG	AGGGGGAA	2160	
AACCAACAAAC	CACCCCCAC	CTAGGGCCAGC	AGCTCACCGA	GAGAGCTGG	2220	
TGACTACATA	GTTCCTCTG	GGATCTTGG	TCTGTCCTT	GGGAGCTCT	2280	
CTATGCCGT	TCCAGGCTGC	ACCAAGGTTT	TGTTGATT	GTCTGGGGT	2340	
CAACTGAGT	GTTCCTCTG	AAACAGGCC	CTTGATTGCG	TGGAAGGAA	2400	
CTTGCTCGA	CAAACATTG	TCAGCATTAA	GTGGCGCTT	TATATCTGT	2460	
GTGTTTTGA	AGCTCTCTC	GGGTACTCGA	CATTAAAGG	AATATCATTT	2520	
TCTGATTATC	CACACAGGAA	ATCTACATCTC	TGCTGCTG	CATGTCAGA	2580	
GAGAAAGCT	TAATGAACT	TTAGTAGAGT	CTCTGGATGG	AGAAACTAATT	2640	
TTGCCGCTT	CTCACTCTG	TCTTTCTC	TCTGGCTAA	TTTCATTTTC	2700	
TTCTGTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGT	AAACATCTCG	2760	
AAGGGAGAGA	TCAGGATTTG	AGGTTAAAG	GTGTTCTG	GGCTTTGAG	2820	
TTCCAGCAGG	GGAGCATATC	GGCTCTGGG	ATCTCAAGG	AAAGATGAGA	2880	
TTGTTGAAGA	ATCTCTCATG	TCTACTTCA	GGCTGTGAC	CATGTTGAG	2940	
TTGACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGGCACAG	3000	
AAACTTTAT	ATCATGTATG	TTTCATCAA	ACCCCTGCAAC	AACTGGGACT	3060	
CTTGTGCT	CTGTGATGT	TTGTGTAAC	TTAAGGGATG	GGAAATATGGC	3120	
CAGGGCTTG	TGGGGCGGT	GGACTAGGCC	CTGGCTATT	TTGCTG	3180	
TCAGGAGCTG	TGCTCTGGT	GGAGGCAAGG	GCTCTGGAGG	GCTATGTTGAG	3240	
GTGATAATT	GGAAAGATGCA	GGACTACTGT	GTGATGAA	CTGAGAAAGT	3300	
ACATCATCAT	TCTACTTGT	ACATATCTC	TGCTGATGCT	TTTCCTCCCTG	3360	
GACTCTTG	CAGGAGGCC	TGCAACAGA	CTGGATGTC	ACCTTCCTGG	3420	
CAAGGTTAC	TTCACTCT	ATGIGATCTG	TTGATACCTG	GTGAGGCTA	3480	
GTGAACACAA	ATTGCTCTC	AAAGGCACTG	CACCTCTTCT	GCTATTGCTG	3540	
CATTAAGAG	AAAGCTCTC	GTAGTTGAG	CAAGGAAAGG	AGATGGAAAG	3600	
TCAGGAGCTG	TGAGGACTA	GGGGGGGG	AGGGGGGAGT	ATAGGGGACA	3660	
CCCACTCAT	CCTCAATTG	TGGAATGGT	TTGCTCTATAA	AAAGTACTTAG	3720	
AGCTCTATT	ACTTCCATT	TCCCAACAGC	TGGCGAAC	GCGGCTGTGAA	3780	
GGCCGAGGCC	GTGTGCGCA	GAGACTATAA	TCCGGCCGG	GGGGGGGG	3840	
CCTCTCTCGT	CTCTCACTG	CGGGGACAT	GTAGAGGCC	GGGGAGACCA	3900	
CAATAGTGT	CTCTCTCTC	TCTCTCTCC	TCCTCTCTCC	ACATAGAAAC	3960	
ACCCGACAC	GGGGCGGAGC	TACCGGGGGG	GCATCGCCG	GGGGCCGGGA	4020	
CTGTCGGGG	GGGGCTCTT	TGGATCC			4047	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAG	GTCAAACATTCC	CCACCTGGCA	CTGTCCTCCGG	AGGGGTGCG	60
CGCGCGGGCG	TGCTGGCG	GGCAGAGGCC	AGAGGCTCTC	GGGGCTCGCC	120
ACCGGGTCA	TGAAAAAAACG	ATCAGTAGTG	TGTTGTTCA	CCGGCGGCC	180
CGGACCCCGC	CCCGGGCCCC	TCGCGGGGAC	ACCGGGGGGG	GGCGGGGGGC	240

TTCTACACT	CTCATGTC	TTCACCGTGC	CAGAGTAGAG	TCAAGCTAA	CAGGGCTTC	300
TTTCCCCGCT	GATTCCGCCA	AGCCCGTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGTA	360
GGGACATGG	GAATCTCGTT	CATCCATTC	TGGCGCTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGACTCA	TAGTTACTCC	CCGGCTTAC	CCGGCCTTCA	TTGATTCT	480
TCACATTGAC	ATTCAGAGCA	CTGGGCAGAA	ATCACATCCC	GTCAACACCC	GGCCGCGGCC	540
TTCGCGATGC	TTTGTTTAA	TTAACACGTC	GGATTCCT	GGTCCGCAAC	AGTTCTAAGT	600
CGGCTGCTAG	GCGCCGCCG	AAGCGAGGCG	CCGCCGCGAA	CCCGGGCCCC	CGGGGCCGAC	660
CCGCCGGGGG	GACCCGGCCG	CGGCCCTCC	GGCCGCTGCC	GGCCGCGCCG	CGGCCGCCG	720
CCGAAGAAGA	AGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GCCCCACAGCA	GGCCCCCGCG	GTGGCCGGGC	CCCGCTCGAG	GGGGACAGTG	60
CCCCCCCGC	GGGGGGCCCG	CGGCCGGGCC	CCGCCGCC	CTGGCGCCCC	GACCCCTCTC	120
CCCCCCCGC	CGCCCCCAGC	CGGCCGTCC	CCGGGGAGGG	GGGAGGACGG	GGAGCGGGGG	180
AGAGAGAGAG	AGAGAGAGGG	CGCGGGGTGG	CTCGCTCGA	ATTCAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAG	AATTCCGAC	GAGGTAGTC	CGGCTCTTGT	CATTGTTGTA	CTTGACGTTG	60
AGGCTGGTA	GCTTGGAAA	GTGATGCGC	AGCGTGTGAG	AGGCGTTGTA	GATGTTCTGC	120
CGCTCAGCG	ACAGCTGGC	CTGCTGGGG	CTGCGGGGT	CCGCATACTG	CAGCAGGGCC	180
TGGTAACTGT	TGTCTTGTG	GAAGGTGATG	ATCTTCAA	CTGTGGCGAA	CTTGGAGAAA	240
ATCTGGTGC	GCACATCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCTACAG	GATCTCTAGC	300
ACGGGGCTC	CGCCGGCTAC	GGGGCTACCT	GGATCCCGAA	GGCCGCCGCGA	GGCACCAAG	360
GCCAGGTT	CCGACTGGAC	CGAGTTTAC	GGCTGCAAGG	CCGGCTGGGC	CCGCCCTGG	420
TTGGGAGAG	TGTCTGGCTT	CAGCTCTGG	TGGTGGAGGA	ACTGGATGTA	GATGGGCTGG	480
CGGGCGACG	CAGGGTCA	CGAGGGTAG	TAGTTCACCA	TGGTATTGGC	GAACCTCTCC	540
GTGTTACAT	CGATGAGG	CTGGGGTTTC	CCCTTCAGCA	TCAGGAGGGT	GGTGAACCTC	600
CCAAAAGGG	GGCCCAAGGG	GATGACTTC	CCCTCCGTA	CTGGTGTGG	GAGCTTCCGG	660
ATGTCGATCA	TCTCTAGGG	GGGGCTGCA	CTTGGCTGG	CTTGGTGG	CTTGGTCTGG	720
TCTTTCGGT	TTCTGCGACA	AGCCGGATTG	CTGCTCATGA	TAACCGTCC	TTTACTGACA	780
CAAGTAGAGA	AAAGCTCGTC	AGATCCCCG	TTTGTACCAA	CGGCTATATC	TGGGACAATG	840
CGGTACATGG	CACACAGG	GAACCCGGG	GGGAGCGAGGT	GGAGGCGCCG	GAATCTGG	900
GCTAGACCTG	CAGATGGAGT	TCTCTGGTA	GAAGGAGG	AAATGATGAGA	GTGCTCTGA	960
GCTGGGGCCG	GCAGCTGAG	CCACCTCTA	CAGCTCTCTA	GAAGCCACAG	ATGCACTGG	1020
TGATGCTT	GCTGACTTC	GGCAAGAATC	CCACAGCTT	CAAGGAGGAAT	TTGGCTACAA	1080
TGCAAGACAGA	CAGAAACATAC	TATGCAAGAA	TGGGGAAACG	CTGCTAGGAG	CCGTGAACTT	1140
CTTGTCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACAGC	TCTACTGT	1200
GAACAGATA	GAGGGCTGCCA	GGCTGAAATA	TATGCTACT	CGAACAGACT	TAGAGGAGCT	1260
GAGCTTACGC	CCCGGGGGATG	CAGGGACACG	TGGTGGACTT	GAAGAGTCCC	AGGCCACTTT	1320
CCAGGGCCCAT	GGGGCAAACT	ATGAGAACTG	GGGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CTCTGGAAAGAA	AACAGAGATA	AGGTGATGCA	TCAGGAGGT	CTGGCTCTTC	ACATGCTGT	1440
GTCCCCCTAC	TTTGTGGGA	ACCCAGAACAA	GTCTGAGGAG	ACCCCTGAGC	AGTCAACAT	1500
CAAGCTCGG	CCTCAGGAG	CTGAGAACACC	CTCTCTGCTA	GAAGGAGCAGT	GAGCTGCTCC	1560
CAAGCCAACACT	TGGCTATCAA	GAAGAGCATC	GGGAAGGGCA	GGCCCAAGGGT	GTGGGAGATT	1620
GGACATGGTA	CATCTTGTG	CACTTGGCT	CTGGCTGG	CTCTTTTC	TGGCTGGGC	1680
CTGACCTGGAC	TTTGGCTAC	ATTCGGATGG	TGGGAGAGG	GGCTGGAGGC	CCAAAGAATG	1740
CTGCCCTGTC	TATCTTCTG	GGCCACAGGC	TTCATTCGA	GAATTTTC	TTCCACTCA	1800
CAGCCAACGG	CTATGACAAA	ACCACTCC	GGCCAAATGCC	ATCACTCTTC	AGGCTGGGGT	1860
GTGCTCCCTG	ACCAATGACA	GGAGCTGAAA	GGGCTGTC	ACCAATGGC	AGTCTCTTC	1920
GAGCTCCCT	GGGGCAATGA	TGTTGGCTCT	AATACCTTT	GTCTCTCCTC	TATGCGTGC	1980
CATTCCAGAG	AAGGGGACTG	GGACAAAGG	GGTGGGGATA	ATGGGGAGGC	CCATTCGCTGG	2040

CCTTGATCT	GAATAGGCC	ACCCCTACCA	TTTATTCACT	AATAACATTTT	ATTTGTGTT	2100
TCTAATTTAA	AATTACCTTT	TCATCTTGT	TGATTTTCT	TCAGCTAAAT	TAGAAATTG	2160
TAGTTTTTCC	CCTAAAAAAA	TCATATGGCAT	TCCTTCTTAT	AAATTACATT	CTCTGATT	2220
CTTGTGACCC	TGCTTCAGG	AAATCCATGT	TCCTAAATG	CTTGTGCGA	CTTGTGCTCA	2280
TACCAATGG	TTGCCTAAC	CAAATATCTG	ACAGCAGAAAT	TGAGCTGATC	CTTGTGAGA	2340
AAGTACGGTT	GAACAGCCAA	GACCACTGGG	TAGTCGAAGA	GAAGACCA	CATCTGAC	2400
TCCCCAGCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCACTGT	TCCTCAGAC	2460
CACTGGTCCC	AAACCAATTG	TCTCTGCCTG	CACTGGCCAA	AATACAGTAG	GAATGCCATC	2520
CCCTTCATAT	TCAGCTTAA	TCCCTAGAGT	TTCATCTGGT	CTCTTATGCG	CAGATGTTAC	2580
TGCAAGTTC	CATGGAAAC	CAAATTTCC	ACAGCGCTTC	TTGATTTTTT	CAACAGTGGC	2640
AGAGTACAGA	GTAGAGCCCA	TCACACACT	ACCCCTCAC	TGACTTTCTG	ATTTCAAAAG	2700
CAACTCTACT	CTCTCTGCAA	CCCACTCAA	GTTTTCTT	ACCATTGGA	GCCCTTCAGG	2760
AGTTCTCT	TTGAGGTGCG	GATAAGACTG	TTTGTGCTC	TGTTGGCTC	GATCTCTG	2820
TGCGCAGAGT	CTCCAGGAT	CATTGTCAT	AAACATCAGCA	AGACAATT	CTTGGTGGT	2880
TACATCAACA	CCAAATTCAC	TCTTCATATC	AACAGTGTA	CAATTCTGG	GCAACCCAGG	2940
TTTCTCCAGT	ATTCAATTA	TAGCTCTGT	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTG	TGAAACACCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCGCCCG	60
CTGCCCGAG	ACATGAGCAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAAGCCG	120
TGACGTCAC	GCAGGACACAT	GGGCTGACT	CACAGAACAA	TTGAAAATAAT	ATACATTATA	180
TATGTACACC	CGGGGGCCCC	AGCTCCCGC	CGTCTCCCG	AGGCTGCGCA	CACCAAGGTC	240
CGGAGGAGGG	GCGGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAGG	GAACAGGAC	300
AAGAAAGGAA	GGAAAGTGG	AAGGAGGGAG	AAATGGGGTC	CCAGCAGCTGA	AATGGAATG	360
AGGTGGGGGG	ATCATAAAGC	AGGAGGAGAC	GATGGTCAG	CTGAGGGAGG	CTTGAGGAGG	420
GGGAAAGGAT	TCCCATGAC	AGGAGGAGAG	AGGGAGGGG	AGAGGAGAGG	GTTCCTCTA	480
ATCCCCCACC	CCCGCCCGAC	CCCGATTCGAA	TGCTCACCT	CTCCCCAACAA	540	
CACTGAGTC	TAAGGGGCGCA	GCTGCTTGT	GGGGTAGAAA	GGCAGCTGAA	GTCCAGGCCA	600
CTTCCACCC	CGCCGACCG	CAGTGCAGG	GGCACACCG	GAGCATGACA	GGCCCGAAAGT	660
GAGGGATGG	GGGGCGGGGG	AGGGCGAGGG	GGCAGCTTCA	AGGGCCCGT	GGGGTTTTG	720
AATGAAAGGA	GGACTGTTT	TGAAACCTCT	CTCCCTCTG	TGCTCTGTTG	TCCAGAAAG	780
TCTCTTCCTC	ATGTCGGAC	TGTCCTGTT	AAACAGGAG	ATTCCCTCT	CTGCTGTTG	840
AGAGGTGTA	GGCTTGTAG	CGGTGTTGGG	GGGTCTCTAT	GATGCGCTCT	TCGTCGCTGC	900
TGGGGGGAT	GGCCACTCTC	GGAGCTGACT	TGCTCTCATC	CTTCCTCTG	CCCCCAACAG	960
CCCCCGTCAC	CAAGGACTGC	CGATTCTGT	AGGACTCTAT	GGGGTTACAA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCAGGAC	AGCTTGTGG	CCTTGGGGTC	ACTGGAGGCC	CCTGGAGGCC	1080
CCCGCGGCGG	TGAGACGGCG	CGGTGAAAGGG	ATGATGGCA	CACCAAGGCC	AGGACGACCA	1140
TAAGGACCCAG	CAACACCAA	TGATGAGGT	TGCGGGGGCTG	GGTATCATGG	1200	
AGTTCTCTG	GGAGCTGCTG	AGGCTGTTG	CGGACCATCTC	AGGGGGGGG	TGTTGACCCAC	1260
GGTGCAGGAA	CTGCTGGAG	CTGACGAGGT	GGCTGGGGTG	GCCAACTGGG	TTCATGCTGT	1320
CGAGGACATT	GAACCTGGAC	ATGAAATTCA	TCTGGAGA	ATGCGGATTC	ATTTCGAGC	1380
AGGAAAGCCG	GAACCTCTG	GTGTTAGAGGG	CAGCTCCGTG	TCGCAGCCGA	TAACGAGCT	1440
GCCTCAAGAT	CTCTTCATC	ACAGTGTATC	TCCTCCACCC	AGCAATATG	AGTAGGGCAG	1500-
ATGTTGTTG	GGCTTCGAG	CGGCTCTGCT	CGAGAGGAGT	TGTTGTCAGG	AGGAGGCTT	1560
CCCGCTGGG	ATCCAGGTC	CCCCCCCCAA	GAGAAATTTC	ACAGGACATTC	AGTTGTTGCA	1620
CAATCTCATC	CGACATGGT	TGTCCTGTC	CTGTCCTGCG	CCAACTCTCA	TCTTTTTG	1680
CCTCCACCTG	TGAGAAATG	GAGCAGGTG	TTGAGATC	AGGAAACAAA	GGAACGCCGT	1740
TGTTCCCTC	AAAGTCACA	GCTGGCGGGG	CAAATGAGC	AGTCGCACTC	AGCAGGATCT	1800
GGGGGGCGTC	AGGCTGAAGG	ACGACACAGT	AGGCCCTCAC	TTCAAGGATG	GAGACCGAGG	1860
ACTCTTCGCT	GAAGCAGCTG	ACAGCAGTGG	TGAGGGCGCA	GGGCGCTGAGC	CCGGCGCTGG	1920
CAAACGGCAG	AGTGTCTAG	TAAGGACCAT	GTCTGAGGG	ATGGTTGAAG	GTCTCCACAT	1980
CATCCCCCTC	CAAGGGTGAGC	AGGGACTGTG	AGGGGTCTAC	GTGGACCTTC	ATGCCTTTC	2040
CCAGGCTCTC	GAATCCCTA	TAGTCAGGAC	CCTCCCGAAC	TGCTACAGGG	CACCTGATGA	2100
CCTCCCGGCT	CTCCAGGCG	CTGAGGCGA	CGCTGAACAC	AGCCAGGTAG	CCATGGAATG	2160
AGTGGTGGAT	CGACAAAGG	TCTCTTGGG	TGGTCTCTG	ACGTTGTCG	CCCTTTCT	2220
TCTCTTGT	CTTCTCTCA	GTCACTGAGG	CCCTAACAT	GAGAGCAGG	TCCCTTCCG	2280
GTGGTGGAT	GAAGGGCATG	TCTATGGAT	GGCGACGGTC	GAAGGAGATG	CCGTCGCGT	2340
AGAGTGTAC	TGTTGGGGAT	TGAGGTTCA	GGAGGTGTTG	GTGCGACTCA	TCATCACAGA	2400
CCTGCTCCAG	CTTCCAGGAG	AACTTGACTG	GGCGGGCACT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAAGCAAT	CTTACAGCCG	TGAGCAGTC	GGCGAGCTG	AGAGAAGCCG	TCTCTATCT	2520
GGACAGCTT	ACATACAGAT	GTTTCTCTT	CCTCTCTGCG	CTTGTGTTGG	GTACAGCCAT	2580
GCTTCATCCA	GAAGGACAGG	GTAGAAGTGT	CACTGGGGCT	GTCTGGGGG	CCAGAGCCCA	2640

GCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	AGTAGATCA	2700
GGCTCTGTC	CTGGCTGTAG	TGCAACCGAGA	GTCTCTGCTG	CCAGTTGGCA	TTGGGGCCAG	2760
GCATGGCAA	CAGATCCTACT	TCCCCCAGTGG	CAGCACCCACA	GAATTTCGGC	AGCCCCCGCT	2820
CTGAGATTT	GTCAACCGTCA	CAGCCCTTG	CCACATGGCT	GGTCTGCAAC	TCTATGGTG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGGC	GATACCAAGG	AAACAAAGCA	2940
AGCTCCCAAGC	ACCTTGGTCCA	TATTCGATCC	TTTGTGTC	GCCTTGCCAC	CTGGGTTTAC	3000
AGGTGGCTT	CAACCTGAATC	TCCACCTCG	CATCATCTGC	TGCCCGGCTC	TTCACCAAGT	3060
CATAAGCTGT	CACTGTAAAC	TTATAGGCGC	TCTCACCACT	GTACTGCAAC	TTCCTCTGT	3120
TCTCAATGTT	CCCGTCAATG	TCATGTGAGA	AAGGGTGTG	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCAG	GCTGTACTTG	GGGAGCAGT	CACCGTCAAT	GGCTTCACCA	CGCAGGATGC	3240
GATCAGTACAG	CTTCCCTCTC	GTCAACAGCG	CACGATCAG	CCGTTCCACA	AAACATGGG	3300
CAAACTCGTT	CACATGTGTG	ACCCGGCAT	GCACAGTGGC	CTTGTGGAC	TTCCTGTGTT	3360
TGGCCCTCGT	GGGGCCCTCG	CAACAGTCA	AGGGCTTGAT	GGTGAAGGTG	TGTTCCCTCT	3420
GGGCTCTCGA	GTCCACAGGC	TCTTGGCCC	GGTACGCCC	CTCTCTGTC	GCCTGTCAA	3480
GGATCACAGC	CTAAAGGGC	ACCCCGAAC	CATGAGCGC	GAAGCCGAG	ATCTCACCTG	3540
CATAGCCGAC	GGGGCATTC	TTGGTCAAGG	CAAAAGTGG	TGGATTCACT	AGGACCGTGT	3600
TGTCTTCTC	CTATGACATC	CCCTGGTACT	TCCTCTCAAT	CTATGGCTC	TGCTGTGTT	3660
CTTGTGTTACA	GGAGCAGGAC	GGGAGCAGAG	AGGCCAGCAG	AAAGGGCAGC	AGCAGGAGGG	3720
TCATGGTGGC	GGCTGGGGCA	GGGGAGGGCC	AGGGCTTGC	CTTCCCTGAG	AGCCTCCAGC	3780
CTGGGGATTC	CACTTGGCGG	GAGGGATA	GGGGGGAAA	ACCAAAATAA	AACTCAAAT	3840
AAATTTGTTA	GGAGGAGTGA	ACCTTGGAGC	CGGGCCAGAG	CAAGGCCAGG	CTTGGGGAGG	3900
GGGCTCTGC	AGGGTCAAGAC	GATCTGCT	GCACACCGC	CCACCTCTGG	AGCCAGTAT	3960
TTTGGCATTC	CTTGTGTTG	AAACGCTG	TCTCTGTC	TGCGACAGAC	CACCGTGTAC	4020
AGGAATCTCTT	CTCAGACAGTC	GTACTCTGCA	TCAATCTCT	TGGCAAAGTC	TCCCTCAGGG	4080
AGACAAAGGT	CTCTCGTAC	CTCCCGCTG	TCTCTGGAGCA	GTGATGTTA	CCCATCCTGG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAG	ATTCGGCACG	AGTGGCACA	TCTATGAACTT	CCAGGCCAG	CCCAAGGCTC	60
AGAACAAAGG	GAAGCTTGTG	CTCTTTGGG	GCCAGAACCC	AGCTCCCAAG	GAGCACGCC	120
CTCCCTCTGA	GGGGCCCAAC	CAGCTCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGCCAGC	180
AGGGTCCAGG	AGGGGCACTG	TCCACCTCTC	AGCTCTGTC	AGTGCCTCCCT	CTTACAGACCC	240
TGGCCCTCTG	GAACACTTGTG	TGTGATCCG	CTGAGCCGGAC	CTACAGCAGCC	ATGCTGTCCC	300
AGCAGGCTGC	CTCAATGAAAG	TGGGCTTCAACT	TCTGATGTC	TCAAGGGCGG	GGCCCGGAGC	360
GTGGGAGGG	TGGGGGTGTC	AGTGCAGCGA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCATTCAC	ATGGAGAACCTG	CAACAGTC	CCCTCTGATC	TGCAACCAAC	GGGAGCCCGC	480
ATCTCTGGAGT	GGGAGTCCCG	ACTTCTATA	ACACCCCTGA	GGCATCTGAC	CGGGAGAAAG	540
CGGGGGGGCT	ACAGCTGAC	CGCTATGTC	GACCAATGAT	GCACACAGAG	GTGCACTGTG	600
AGGTAAGGGC	CCCCCAGGCA	CCCCCTGAATT	TCTTCAACGC	AGCCAAAGAAA	CCCCCAAAACC	660
AGTCTGCTC	CTCTGCAACCC	TTCTTCACTG	CTTCTGGCCA	CAAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCCACCCGG	CCCCACCCGG	TGGCTGCCCT	CCCTCCACAG	AAGCACGCC	780
AGCAGCAGCA	ACACACGAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCG	840
TCTTCTGAGA	CTCTCTTC	ATGGCCACAG	ACCTCTGGCA	GCACACCCAG	GACTTTGCC	900
TGCAAGGCG	TGGGGCACTC	GGAGCTCCC	ATCTGGCTCA	CCACAGCATC	GCACCTTAC	960
CTCTGGCTCC	CAACCCAGAT	ATGGACCCAG	AACTCTGCCAA	GGCCCTCTCTG	CAGGACTCTAG	1020
CCCCCGAGCG	AGGGCTACTCT	CAGGGCTCAGA	TCCCTCTGCC	CCCGGGCTCC	CCCGGGCTCT	1080
CTAAGGAGGG	TATCTCTGCC	CCACAGGCC	TGGATGGGGC	TGGCACCCAG	CCTGGCCAGG	1140
AGGCCACTGG	CAACCTGTTC	CTACATCAGT	GGCCCTCTGC	GCAGCGGCCA	CCTGGCTTCCC	1200
TGGGGCAGCC	CTACCTCTGAG	GCTCTGGAT	TGGGGCTCTG	GCCTGGGAGAC	TGCGACGTAC	1260
TGCTCTGATGG	GGAGAGACTA	GCACCCAACTG	GGGGGGAGGC	AGAGGCTCTC	GCATGGGCA	1320
GGCAGGAGGG	CATGGAGGCC	GTGAGCACAG	GGGACTGTGG	CGAGCTGCTA	CGGGGGCGAG	1380
TGATCCAGAG	CGGGCCAGCG	AGGGGGCCGGG	CATCCCGAGA	GGCCAAATTG	CTGACCTCTG	1440
CCCCAGGAGC	TGTGAGCTG	GCCTCTACTGC	AAAGATGCAA	GGATGCGAGT	DTGCTCTGAAG	1500
AGAACCGGAA	AAGTGTATTG	GCCTCAACTA	CAAGTGTGG	GGTGAGTT	TCTGACCCCTT	1560
CCTTGGCCAC	CAAGCGAGCA	CGAGAGACA	TGGGGATGGT	ACCCCTCATC	ATCCCACTGT	1620
CTGCTCTGCT	GGCAACTGTG	GACCCAACTG	AGGCAGCCCA	GGCTGGAGGT	CTTGTATGGG	1680
ACGGGAAAGG	TCTTGAACCTG	AGCAACAGGC	ATCATGCTAC	GTCAACCCGA	1740	
GGCGGTCTAC	CGGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGGGAGGAC	ATGATGTTCA	1800
AGTGGGGAGG	GGAGCCCTGGC	GTGGGAAACAA	CAAGACAGCG	GGCCAGGCC	GAGCCCTCTA	1860
TCATCCCTCA	CAACGGGGCC	ACTTICATCG	CCCCCTCCGGT	CTACTCAAC	ATCACCCAT	1920
ACCAGAGCCA	CCTGGCTCT	CCCTGGGCC	TAGCTGACCA	CCCCCTCTGAG	CGGAGCTTGT	1980
AGCTACATCTC	CTACACGCCG	CCCCCCATCC	TCAGACCTGT	GGGGGAAGGC	TCTGGCTCT	2040

ACTTCAATGC CATCATATCA ACCAGGACCA TCCCTGCCCC TCCTCCCATC ACGCCATAAGA 2100
 GTGCCCATCG CACGCTGTC CGGACTAACAA GTGCTGAAGT AACCCCGCT GTCCCTCTG 2160
 TGATGGGGGA GGCCACCCCA GTGAGCATCG AGCCACCGAT CAACGTGGC TCCGGTTC 2220
 AGGCAAGAAT CCCCTGTATG AGGGACCGTG CCCTGGCAGC TGAGATCCC CACAAGGCTG 2280
 ACTTGGTGTG GCAGCCATGG GAGGACCTAG AGAGCACCGG GGAGAAAGCAG AGGCAAGTGG 2340
 AAGACCTGCT GACAGCCGCC TGCTCCAGA TTTCCTG TGCTGCACCC AACCGGAGC 2400
 TGGCCCTGCA CTGTCGTGAC GAATCCAGAG GAGACATCTT GGAAACGCTG ATAAGCTGC 2460
 TGCTGAAGAA GGCCTCTGGG CCCACAAACC ATCCGCTGGC AACTTATCAC TACACAGCT 2520
 CTGACAGTG AAAGATGCCG GAGAGGAAGC TGTTCAACAA AGGCAATTGCC ATCTACAGA 2580
 AGGATTTCTT CCTGGTGCAAG AAGCTGATTC AGACCAAGAC CGTGGCCAG CGTGGTGGAGT 2640
 TCTACTACAG CTACAGAAG CAGGTGAAAAA TGGCCCGCAA TGCGACTCTA ACCTTTGGGG 2700
 ATGGTAGATC GAGCGATGAC AAAGTCGGCC AGGGAAAGGTT TGAAAGTGGAT ATTAAAGACTT 2760
 CCAAAGAATG CTCCTTCAGA GAAGAGAAGTC CCGCAAGTGAAGAGCTGG 2820
 AGCCCAAGAG GGAGGTGAAG GAGGCAAGGA AGGGAGGGGA GGAGGGAGTC CCAGAGATCC 2880
 AAGAGAAGGA GGAGCAGGAA GAGGGGGAG AGCCGACAGC CGGGGAGGG CGACTAAAG 2940
 CCACGAGAC ACTACAGGCC AATGAGTCGG CTCAGTACAT CCTCATCTC CGGAGCCAGC 3000
 AGTCCCAAGCC CTCCTGGCT CCGGTGGCC AGGCTCGGA GAAGCCAAGG GAAGGGACAG 3060
 GGAAGTCAGG AAGGGCACTA CCTTTTACG AAAAAAAAAA AAAAAAAACAA AAAGCTT 3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAACTCGGCA CGAGGCTGAGT TTCCCTGTTGA ACACAGAGGC TGCCCTGTC ATTACAGACAA 60
 CGACGGATAC AGACCGAGCT TGCTCTATAA GGATCCCAA CAGTGGATT GTTGTAAATC 120
 TTAATCCGCT AAACAGTTCG AAAGGATATA ACGTCTCTGG CATTGGGAAG ATTTTTATGT 180
 TTAATGCTG CCGGACCTGCT CCGTCTGTG GGACCATCTC GGAAAACCTC GCTTCTGGCT 240
 GTGAGGCGAGA AACCACAAAGA CAGGAGCTCA AGATTTGGAA GCAGCAAGG CCAGCTGGAA 300
 TTGAGGAAAGG CTCCTGGCTG TCCACAGAGC GTCTACATCAG TCTGACCTAC AAAAGGCCCTC 360
 TCTCTGCCAA AGGTACCGCT GATGCTTTA TGCTCCGCTT GTTTGCAAT GATGATGTT 420
 ACTCAAGGGCC CCTCAATTC CTGCACTAAC ATATCGACTC TGCCCAAGGGG ATCCGAAACA 480
 CTTCTTGAAGG GTTGAACACG GGGTGGCTG GTGTTCTTC TCCAGTGGG TGCCAAGTCA 540
 CCGACCTGGC TGGAAAGATC TAGACCTGA TGCGCTTACG CACAGTCAGG AAACCTTGGG 600
 CGGGCTGTTG CACCTCTGTC GATGGGAGAA AGAGGACTTAC CTATTTGAGG GTTGTCAATC 660
 CTCCTCCCTTA CATTCTGGCA TGCCAGGGCA CGCGACTGGG GTCTTGTCTTA GTGTCAGAG 720
 GCAATGCTG GAATCTGGT GTGGTGCAGA TGAGTCTCCC AGCCGGGGGG AATGGATCTT 780
 TGAGCATCAT GTATGTCAGG CAGGCAAGT TGGGAACTC CGCCCTCTCC ACCAGGATCA 840
 CGTTTGTAGTG TGCTCAGATA CGGGCTCAC CAGCATTCA GCTTCAGGAT GTTTGTGAGT 900
 ACGGTTTATG CTGGAGACTC GTGGAGACCT GTGTTGCTT CAGAGTGGAA GGCGAACACT 960
 GTGAGGTTGAA AGACCAAGC CTGGCAACT TGTATGACCT GAAGGCTCTC GGCGCTCAAG 1020
 ACACCATGTT GAGGGCTGGC ATCACTGGCA CGGGGAGGCC GGAGGACTAC TCTACATGTT 1080
 CAGACCTGTG CCCCCAACAGT GACAAGTCGA AGGTGGTCTC CTCTAGTCAG GAAAAGCGGG 1140
 AACCCAGGGG ATTICACAAA GTGGCAGGTC TCTGACTCA GAAGCTAATC TATGAAAATG 1200
 GCTTGTAAAG AATGACTCTC ACGGGGGGGG ACACAGTGGCA TAAGGTTTAT CAGCGCTTCA 1260
 CAGCCATCTT CTTCCTACTGT GAGGGGGGGCA CGACGGGGC AGTATTCTCA AAGGAGACTT 1320
 CAGATGTTGCT CTACTTGTGTT GAGTGGGGCA CGGAGGCTTG CTGGCCACCTT TTGATCTGA 1380,
 CTGAATGTTGCTTCAAGGATGCTGGCA ATCTCTGGCA CCTCTCTGCTC CTGTCAAGGT 1440
 ACAGTGACAA CTGGGAAGCC ATCACTGGCA CGGGGAGGCC GGAGGACTAC TCTACATG 1500
 TCTGCACTGCT CTGGCTCCAGG CAGGGCTGGCA TGAGGCTGGC CCTCTCAGAA GCAGCGGGT 1560
 GTCCTGTGG TGCGCTCCAGG CGCGTGAAAC TGCGCAGGGT AAGGGACGGG CCTCACTGG 1620
 GAGATGGCAT AATGCTCTG AAATACGTTG ATGGCGACTT ATGTCAGATG GGAGATTCTGA 1680
 AAAAGTCACAC CACCATCGCA TTCACTTCGA CGGAGGACCA AGTAACTCC AGGCCCATGT 1740
 TCTACAGGGC CTGGGGAGAC TGIGAGTACA CCTTTGGCTG GCCCACAGGCC ACAGCCCTGC 1800
 CCATGAAGAG CAACGACGAT GTGACTGCC AGGTGCAACCA CCCAAGCACA GGACACCTGT 1860
 TTGATCTGAG CTCCCTTAAGT GGCAAGGGGG GATTCAACGG TCTCTTACAGC GAGAAGGGGT 1920
 TGGTTTACAT GAGGATCTGT GGGGAGAATG AAAACTGCCC TCTCTGGCTG GGGGCTCTG 1980
 TTGGACAGAC CAGGATTAGC GTGGCAAGG CAAACAAAGG GCTGAGATAC GTGGACCAAGG 2040
 TCCCTGCACT GTGTACAGG GATGGGTCTC CTGTCCTC CAAATCCGGC CTGAGCTATA 2100
 AGAGTGTGAT CAGTTCTG TGCAAGGGCTG AGGGGGGGGG AACCAATAGG CCTCATGCTCA 2160
 TCTCCCTGGA CAAGCAGACA TGCACTCTGT TCTCTGGCTG GCACACGCC CGGGCTCTGG 2220
 AGCAAGCAGC TGAGTGTCTC TGAGGAATG GAAGCTCTAT TGTTGACTTG TCTCTCTTA 2280
 TTCACTGGCACT TGAGTGTCTG TGGAGCTTATG ATGAGAGTGA GGATGATGCC TCCGATACCA 2340
 ACCCTGATTCT CAATACATAT ATTGTGCAAG CAACTACTTACG TCTGACCGGA GTGCCCTGTC 2400
 CTGCCGGAGC CGCTGTGTC AAGATTCCTA TTGATGGTCC CCCCATAGAT ATCGGGGGGG 2460
 TAGCAGGACCA ACCAATACTC AATCCAATAG CAAATGAGAT TTACTGAAAT TTGAAAGCA 2520

GTACTCTTG	CCAGGAATTG	AGTTGTAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCAT	ATCCTGGTC	ATTGTCTAC	AATTAAACA	ATGGTCAGC	2640
TACCGCTTG	TAATTITAG	GGACTGCAA	CAAGGCTTT	TCTTGAAGCT	GAACCAAAA	2700
CAACTCTTA	TGTTCTTAG	GTCTTGAAT	ATGTCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAATTG	GGTCTCCACC	AGTACCAAT	GCAATCGCA	ATGACCCAGT	CTTGCACAAAC	2820
TCCATCTGA	CGACCCAGTA	TCTCTGTAT	TAAGCGTTT	AGTCTTCTAA	CTTCATCTTC	2880
TCCTGGTTA	AGTTCACAC	CAGGTAGTT	GAAGAAAGTT	GTTCCTTCACT	GCAGCACTAA	2940
CACATGGGG	AGCCGGTGT	CATGTACAT	CAGAACCCCT	TCTACAGTCC	TCCTCATTC	3000
AATTATTC	AATCTCTCC	TCATGCCGT	AAATCTGGCT	GCAACAGAGC	TGCTCTTCTC	3060
GTAGAGGGG	TCTTTTGAC	CAAAGATTA	ATTTGAAAGA	GGTGTACAGGT	TGATGTTGCG	3120
CTCCAGGGG	AGGGGCTTGG	TCTGCTGGAT	GTACTTGTG	CCGAACTGTAG	TGACCCCCGG	3180
GGGCCAGCG	GTCTGCCAGG	GATIGGGCGG	TACACAGACG	ATGCTGGCGA	GCTCCGGCGC	3240
TGACGCCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTCCC	CGTGCAGGAA	GCCTCGTGC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCCGCA	CGAGAAATGGA	TCAACCTCAA	CAACACGTTA	AACTAGACG	AAAGAAAGTA	60
TACACAGTG	ATGAGTCCTCA	CATGAAATAAC	CCGGATGTAA	ATCCAAAGAA	ACAGGAAGCA	120
GAITGGGGT	TGCCAGGGAC	AAGGGCGGTG	GGAGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTTGAG	TGATGAGAT	GTITGGAGC	TAGATAGAAG	TGTTGGTTG	ACACATTGTC	240
GGATGACTA	CCACTTAAAT	GTCTACTAA	AAAGTAAATT	TATGTGAATT	GCATCTTAA	300
TAAAAAAAGA	GATAACATTC	CAACTCTTGG	ACATTATCT	TCTCTTCCAT	TTGATGTCAG	360
GCCCGTTA	GAATTCAT	CCGGTTTGG	CACTGCACTT	AAAGATGTGG	GAATTAAGGA	420
CGCACAGTTA	AGAGGAAGGA	TAACATCTGAT	TAAGGTAGTC	CTTCTCTAGG	TTTCCCTTAA	480
ACAATTAAAC	AGATGGATAG	TGGCACCACT	TACCGAGATG	AAAACCCAGC	GGAAAGGAGA	540
TTTGGGGGAG	AGTGTAAATT	TGTCTGGCC	CTGTGTTTG	CAACCTGAGT	GTAAAAGACA	600
TATGTAACT	CTTCAGTGG	GAACACATA	AACTAGAAAT	GTATCAGAAT	TTATCTTTC	660
GATGACTG	CTCAAGATG	GTCTGTCG	TCAGTGCCT	GGTCAAATGA	CAAGATGGCC	720
AATCTTTC	TGAAGGTCCT	AGCACCTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTGCT	780
TAGAACATC	CTAGTTCATG	CTTATGTC	CTCATGTAAT	TAATATCCT	CTCAAAATGT	840
CTCATTTGT	GCATAATT	CTGCAACGT	ATGGCGCAG	TCTCGGGCC	CGAGGGCCG	900
GACCTTGT	TGCGAAAAGA	GGACCATCCC	ATGAGGAGA	AAATCATGG	GAACCAATTC	960
TCTGCAAT	CTGCGCTCA	TCACAGGAG	TTCAACAGG	GGCCCGGGAA	GGCCAGGCTC	1020
AATCACTG	ACAGGGGGC	ACTCAAGCTG	CTGCCCTGC	GTACACAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGCTGGC	ACAGGTGA	CTACGGCTG	TGACCGGACCC	TGCTCTATGAA	1140
GATGTCACAA	ACTGTCATG	GAAGGGCTTT	GTGTCATG	ACAAAGATGCC	TGCTCTGTG	1200
CTAGATTACT	GGCAGTCTCT	CATGGACAG	GGGCGCTGA	CACACACCCG	CCGCACCTTC	1260
GACCGTCCC	TCCGGGCATC	CGACGATCAGC	TGATGTCAG	GAATTGGCC	CCTGTATCTG	1320
CGCTTCTCG	GTCTCACAC	ACTGCTGTG	ACAGCTGTG	GAGGCTATCG	GGCTCTCTC	1380
AAGCTGAGTC	CTAGAGTGC	AGGGAGTAC	ATTTGAGTAC	TCAAAGTCAG	GTACGGGCTG	1440
GATGAGGCC	CGCCAGGGCT	GGCCACCGTG	GTAAAGACG	AGCCCTTCTG	GTCTAAGGCC	1500
GGCAAGTCCA	ACTTACAGCT	GTGCGACGAG	CTGTCGACCC	TCATCTCCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATG	GGACGCCATC	ATCCGGGGG	GCCTCACCCG	CTTCACCGAC	1620
CAGCTGGCG	ACGCTGGGT	TCTCTGCGG	GACTACTAA	TCCGCAGCG	CCATTTGAG	1680
AAGGCTGGG	ACGGTGTGAG	GGGACCCATC	CGGACAGTGA	TGACCGTGG	GGACCTTCACA	1740
CAGGTGTTG	ACAGCTACCG	CCAGTGTGAG	GAAGAGATGA	TGCTGTCAA	GATGGACACC	1800
GCTCTGGAGC	TGGGGGGCGA	GGGGAGGAGAT	GATGTGACCA	TGAGAGCTGG	CTGGCCCGC	1860
TTGAGGAGG	TCATCAGGCC	GGGCCCCCTG	CTCTCAACA	GGCTTCTGCT	GGCCCCAAAC	1920
CCACACCCG	TCAGCAGGTG	GCACACGGT	GTGCCCTGC	ACCAGGGCCC	CCCCCGGGAG	1980
ATCATCAAC	CTTACACAGA	GGCTGTGCA	ACGGTGTGAC	CCCTCAAGGC	CACAGGCAAG	2040
CCCCACACTC	TGTGGGGGG	GTTCGCAAG	TTTATGAGG	ACAAACGGAA	GCTGGACAT	2100
GCCCGTGTCA	TCTCTGGAGA	GGGCAACCAAG	GTGAACTTCA	ACGAGGTGGA	TGACCTGTG	2160
AGCGTGTG	GTCACTGCGG	AGAGCTGGAG	CTCCGACAGC	AGAACATCGA	TGAGGCTCTG	2220
CGCGCTCTGC	AAAGGCCAC	GGCCGTGCT	GGCCGGCCGG	CCGAGTACTT	TGATGGTTCA	2280
GAGCCCGTGC	AGAACCGGT	GTACAAGCTA	CTGAAGGCT	GTGTCATGCT	CGCCGACCTG	2340
GAGGAGGCC	TCGGCACCT	CCAGTCACCC	AAAGCCGTG	AGGACCCAT	CTTGACCTG	2400
CGTATCGAA	CACCCCGAC	CGTCATCAAC	TATGCGAC	TCTCTGGAGGA	GCACAAAGTC	2460
TTGAGGAGGA	GTCTCAAGGC	GTACGAGCGG	GGCATCTCGG	TGTCATGAGT	GGCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CTGACCAAA	TTCTATGCC	GGTATGGGG	CGCCGAAGCTG	2580
GAGCCGGAC	GGGACCTGTT	TGACAGCTG	CTGGACGGCT	GGCCCCAAAA	ATATGCCAG	2640
ACCTTGAC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGG	GGCTGGCCCC	GCATGCCATG	2700
GGCGTGTACG	ACGGCTGCCAC	CAGGGCCGTC	GAGGCCGCC	AGCAGTATGA	CATGTTCAAC	2760

ATCTACATCA AGCGGGCGCG CGAGATCTAT GGGGTCAACC ACACCCGCGG CATCTACAG 2820
 AAGGCCATTG AGGTGTCGTC GGACGAGCAC CGCCGCTGAGA TGTGCTCGG TTGAGCAC 2880
 ATGGAGTGCAGA AGCTGGGGGA GATTGACCGC GCCCCGGGCCA TCTACAGCTT CTGCTCCAG 2940
 ATCTGTGACC CCCGGACGAC CGCGCGGTGAGA CCGAGAGCTG GGAGGGACTT TGAGGTCCG 3000
 CATGGCAATG AGGGACACCAT CAAGGAAATG CTGGGTATCC GGCGCAGCGT GCAGGGCCACG 3060
 TACAACACCG AGGTCAACTT CATGGCTCG AGATGCTCA AGGTCTCGG CAGTGGCCACG 3120
 GGCACCGTGT CTGACCTGGC CCCTGGGAG AGTGGCATGG ACCACATGAA GCTGCTGAA 3180
 CAGCGGGCAG AGCAGCTGGC GGCTGAGGGC GAGCGCTGACG AGCCCTTGCG CGCCCAAGAC 3240
 AAAGATCTGTG TGCTGAGGGAG TGACGCTCC CGGGAGGAGC TGCGAGACTG CGCACAGAG 3300
 GTCAACCCGG AGGGAGATCCA GCTGGCCGAG GACGGAGGAGC AGAACCGAGAT GGACCTGGAG 3360
 CCCAACCGGG TTCGCTGGA GCAGCAGAGC CGCGCCAGCG CAGTGTGTTG GAGGCTGAAG 3420
 GAAGACTGAC CGGTCCCCTG GTGCCGAATT CGCGCAGAGC AAACCCAGCC CCCAGATCAT 3480
 TTGCGCTCAA GGTTTTCCTG CGAAGTCACA AACGTTTCAA GGAATCTCAA ATTTCACAAA 3540
 GTTTGAATG TGCGATTTGG TGCGCTGTG CTGTCGTC CTCCTGTA GCTTTTCYCC 3600
 CTACATCCTT GAAAGGATGG TGAGGCTCTG CCTCCCTGGC CAGACCTCCCTTCCAGCGC 3660
 CCAGGCATG GGGTGTGAG AGGGCAGCAT GTCTAGGTG ACCGTGCTCC TGCGCTCCAG 3720
 GCGCGTGCCT CGCTGTCCTC TAGGCCACTA AGGGCCCTGGC CCATTGTTGC TAAACAGCGA 3780
 GTCGGACCTA GAAAGAGCAG AACATCTCTC TGGGTCACTA CTCTGGCTAG GAGCTGGCT 3840
 CCTGACTGGT ATCCAGCGCT TCTCCCTGCA CCATGTAAT TCCCGAGGGC AGACCTGAA 3900
 ATGTTGAAACA CAGCACTGGC AAAGAAGATG TAACCGGGGG ACCGAGGGCT CTCTCTCT 3960
 CCTGCTCTG TTCTGTTGGT CAGAGTAGCT GAGGGCTGTG TGAGGAGGT TGAGGTCTG 4020
 GTTTTACCCG TGTTGTTGGT GTCTTGTCTG GAGGGCAACTT AGAAAGGCCCA CGCCAGCCCT 4080
 TGCTCTGGC CTGACACAG CGAGGGCAGT TTCTAGGTA TGCTCTTGAT TTCTGAGAA 4140
 GCAGCAGTGC CATGGAGCC AAGAGGAAGT GTGACTGAAA CTGTCACACT ATAGCCGGC 4200
 TGCGTATTG AGGGGGT 4218

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCCGGC GCTCTGCAAGT CGAGCTACTAGT GGATTCGGCAAG ATTTCGGCAAG GAGGGAAACT	60
CAACGGGTGA CGAGTGGGG ACAGGGACAG CGACCTCTGT GTGTGAAAGCA CCCACACCTCG	120
AGGAGCTCTG TGAGCAGGTG CGACAAAGATG CGATTGACTG GGCGGACTTT GGGGTAGAGG	180
CACTGGCTGA GGGGAGACTG TCTGGCATCT CGCGCAGGGC TGCTGGAATC GACTGGGGCA	240
TCTCCCGGA ATCAGATTC AAGGATCTCG GAGGGTGTG GATAAGCTTG GGAGACGATG	300
CTGTTGGTCA GCGAGATCAGA CTGTCGAGG CAGGAAGCTTCA GGCCTCCAGAA GTTGTGCA	360
GGGGCCAGAGA TGCGCTGACA CTGCTGTGAAT AACACTGAGAC CGGGAATCATG TCTCTGTATG	420
AGCTCATGGA GCTTGTAGTC TTCTTGTAGCC AGAGAGCAGT GGAGTTGAGT GAGGAGGCAG	480
ATGTCATGTC TGTGAGGCAAG TCTGGCTGTG CTCCAGGGCAT CTCAGGGCC CAGACCAAG	540
AGAAAGATGGT TACCAATGGTG TCAGTGTGTT AGGATCTGAT TGGCAAGCTT ACCAGCTTTC	600
AGCTGCAACA CCTGTTTATG ATCCCTGGCTT CACCAAGGTA TGTTGGACCGA GTGACTGAAT	660
TCTCTCAAGCA AAAGCTGAAG CAGCTCCAGGC TGCTGGCTT GAAGAAAAGA CTGATGGTG	720
AGAAAGCAGCA GGAGGAGCTG GAGGGAGCAG CGCGCTGTGAGA GGCCTAAAGCTG GACCTGGCTA	780
TGAGGAGACCA CAAGGGCTG CAGAGCTGTA TTGAAGCTGA CATCTCCAGA AGGTACAGCG	840
GGCCGGCTGT GAACCTGTG GGAACCTCTC TGTCGACACC TCCTGTGTTCT TGCTGCGCA	900
TCTCTGGCTG TTCTGGATG AGAGTATGAG CGACGGCTGT TGTTTTGGGG CCCTCTCAAGG	960
CAAAAGACCA GGCTGACTGTG AACATGGAAA CGACGGAGAA GGAAAGGCCA CCTGATGGTG	1020
ATCTTGGCAGC TCTCTGATGT CTCTCAAGA AGCTGTTGGT ATTGGCCCTG TGTTCTATCA	1080
GGCGAAAGAACAC ACAGATTCTC CTCTAGGTA GTATAGGCC AAAAGCTCT CGAGAGTACT	1140
TCTAGAGCGG CGCGGGGGCC ATCGATTTT CACCCGGGTG GGGTACCT 1187	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA AGGGAAACAAA AGCTGGACT CGCGCGCCCTG CAGGTGGACA CTAGTGGATC	60
GAAAGTTCTG TACGCCAACG TCGAAATTAA CTCTGGGCTG ACCCATAAAC ATTGGTCTGA	120

TCTAGGATAT AGTTGCCTT CTTGGGGCCA GCAATCTGGA TGAGGGCGTT GAGGCCACTGG 180
 GTGGCCTGCT GGATCAGGGC ATCCAGCGG CCAGCATAGT TCCGCTGCC CGCTAGGCC 240
 ATCACCCGCA TCCTATCCAT GATGGCATTG GTACCCAGGA TTGTGTACTT CTTGGAAAGGG 300
 TTGGAGGCTG CATGGTGTG GCACCATGTC TCTGGCGAG CAGCAGGAG CCCCCACATC 360
 ATCAGAATCT CACATTCTGC CTGGCTCTT GTTCCAAAGG TGCCCCCGGAT ACGCTCACTA 420
 AGGGGAAGGT GTCTGGATGAA GTTAAACCCC GGAGGACAG AACAGTAGGG CTCTGCTCTC 480
 TGTCGAAGT TGAACCTCAC TGCGCAATT TCACCCAGGA CATGAGGATA GAGGGCCTGA 540
 CCCCCCAAGT CTTCCTCTTG GATTCGGAAAG GCAATGCCA TCACTTTCC ATTCTTGTGA 600
 AAAGACAGT CCACGCTATT TCACATTC AAATCCGCA AAGCAGCAAAT CACCGGAGAG 660
 CTCTGGCTG CTAGGAGAGC GGCTGGGCC CGACAGCTGGG GGGAAAGGTC CGCAGGCCA 720
 GTGGGGCCG GAATCAGGGC CGCGCTGGCC TGAGGAAAGCC CAGCTCTGGC TGAGGGGG 780
 GCTGACAGT GTGGCTCTG GTTCCGGCCC GGGAGCCTG CGAGTGTGCG GCCCTCGGGT 840
 GGATTTCTG AGCACCAATA CTCACGGTT GCGAACCTGG GGTTTTAACTG CCTCTTGTGTT 900
 TAATCCCTCA GGGGGGGCTG GGGGACCGG GGGGACGGAT GGGCAGCTGG GTGCAATCTC 960
 GCTGTAACGG AGCCATTCTA TGATTTCTTA GAATTAACTA AACGGCTGCC CGGGAGGCCG 1020
 CGGGGGCCGG AGCGGAGACG CGCGCTGTA TGCGCTGGAG TGCGCTGCC GGGGCTGCC 1080
 TCCCGCCGGG GGACCCCGG CTCTGGCCG GCGCCGCTCCG GCCTCCGGGG GGCCCGGGC 1140
 CGCGGGGACG TGTTGGCTGT CGGACCCCTT CCCCGCCGGC GTTGAACCTCC CGGGCCGGC 1200
 CGGGGCTGG ACGTCGGAGC GGGAAAGATGT TTTCGGCCCT GAAAAGCTG GTGGGGTCCG 1260
 ACCAGGGCCC GGGGGGGAGC AAGAACATCC CGCGGGGGCT GCACTTCATG AACCAAGGGT 1320
 TGCAAGGGC CTTCGGCAAG GGGGTGCACT GAAACATGAA GATAGTGTAC CGGGGAGACA 1380
 GGAACACGGG CAAGACAGCG CTGTGGCAC GCGCTGAGGG CGGGCCGGTC GTGGAGGAGT 1440
 ACATCCACAC AGACAGAGT CAGGTACCA GCACTCAACTG GACCTACAAAG ACCACGGATG 1500
 ACATCTGGA GTGGTAAAGC TTGGATGTAG TACACAAAGG AAAATCCTAA AAGCGAGGCC 1560
 ACGCGTTAA AGTGGAGAC AGGCCCGAC AGNCAGGAGC TGAAATGCC CGGGATCTG 1620
 AGTTCTGGA CGTGTACAGC ACTYGCACAG GGGTGTGCT ATGTTTGAC ATTACCAAGC 1680
 AGTGGACCT CAATTACATT CTCCGGGAGC TTCCAAAGT GCGCCACCCAG GTGCCGAGT 1740
 GCGTGTGGG GAACACTGG GACATGGCC AGCAGGAGT CATCTGCCG GACGACCTGC 1800
 GTGACTTCAT CGACACCTC GACAGACCTC CAGTTCCTC CTACTTCCG TATGCTGAGT 1860
 CTTCATGGA GAACAGCTTC AGCTTCTATAA GTTCTTCAT GATCCCTTTT 1920
 TGCACTGCA GAGGGAGACG CTGTGGCCG AGCTGGAGAC GACAGCTGG GACATGGACG 1980
 CCACGCTGGA GGAGCTGTG TGCGACGAGG AGACGGAGGA CGAACACTAC GGCACTCTCC 2040
 TGGAGATGAT GGAGGCTGCC AGCGCTGGCC ATGCGCTCCC ACTGGCGGCC AACGGGAGA 2100
 GCCCCATCCC GGCGCTCCAG TCACCGATCC TGCGTGCACC CGCTGTGTC ACAGGGAGCT 2160
 CCACGGCCGG CAACACCCAG AGCTGGCCCT AGCTGTGCC GCAACCATCTT 2220
 CTGTCGGCCC TGACACCCAC TCAGAGGCC CGGGCCACCC TGCGTCCCG TCAGGGCCCG 2280
 CCCACGGG CACATCATC TCTGGCTGT TTGGAGGCTC ACCTGGCCAC GAGGAGGCC 2340
 CTCCACCTC AGACGGACTC CGGGCCGGAC AACGGCCAGC AACGGTCCAG AGTGTGGAGG 2400
 ACTTTGTC TGACGACCCG CTGGACGCCA GTTCCCTGGA AGACACAAAC CGGGCCAGGG 2460
 ACGAGAAAGA GTGGGGGGAC AGCGATGCC AGCAGGAGT TGACAGTGT GGGGAGGCC 2520
 TGCGGGCCTA CCGGATGTCG CGAGGGTCC AGACGGATGT GGACCTCGAA GACCAAGCC 2580
 GTGGGGAGTCC CGCGCTCTC GTCCGGCTGC AGACATCACT CTTTGAGT 2640
 AGGAGGAGC AGAACTGGCA AGCGCCACCA AGGCGCTCC CGCACTGCT CGCAGCTG 2700
 CAGACCCAGA GACCAATGG TCCTCCATAC CAGCTTGAA GCACAGGGAGG GGGACAGCTC 2760
 CCACGGAGG CGCAGACCC CGCTGGCCAG GCCTGTCTC TTGTCGACAA GTCGGAGAGA 2820
 AGCGCAGCAG CACCGAGCC CTCGCTGAGA TGAGGGCGG GAAGGGTAG CAGGCCCTCT 2880
 CGTCGGAGAC GACCGGGACG CTGACCATG CTGACAAAT GTGTCCTTC GTCATGGATG 2940
 ACCCGGACTT TGAGACGGAC GGATCAGACA CAACGGCAG GCGCGATGAC TTTCCCTG 3000
 GAGATGGAC CTGACATGTG ACTGGGGCC AGTGGGGGCC TGCGGAGGCC CCCCAACCCC 3060
 CCAAGCTCCC TCTCCCGGC TTCACTGTA AGAATGACTC GCAACCTTC CGGCTGGGG 3120
 TGGAGGAGG CGGACCCCAAG GAGACAGTG AGGAAGGTAAG GGAAGGCAAAC ACCCCCTCTA 3180
 AGGAGAAGA AAAAACACAA AAAAGCTCT CGAGAGTACT TCTAGACGG CGGGGGGCC 3240
 ATCGATTTC CACCGGGTGG GTGACCGAGG TAATGTGACCA ATTCGCCCT TATAGTGAGT 3300
 CTGATT 3306

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCCA GAGTGGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCCTGG CCTGCGGATG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTC GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCCGT CTCCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCCTC CCTGTCACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCG AGAAATTCA

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAACACCTATG GTTACAATTG

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTG GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCCTCC GACGCCCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCATTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCACGTGGGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTTCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCCTGGTCC GCACCAAGTC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC CGGTCAACAC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGC GTTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTCAGAT GCAACGCCAG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGCACA CAGAGCAGAC

20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACCGATA GAGGAGAGAC

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCACAT TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCAACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGCTTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCACGAC

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAATGAGG TGGGGCGATC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTGCCCTG GACAAGGATG

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGGAAGCC ATTGACGGTG

20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGGTCTCTC GTCGCTGCTG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCC CGCACACAC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTG CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTATC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGGAGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20.

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGAATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTTAG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCGCACAG

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTTC TGTTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGGCCCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCAC TG

20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGATGAC AATGCACCAAG

20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG

20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCTCTATA ACCACCAAGTGT

20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACCGT GACAAGTGTG

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTTGGAT GTACTACCA

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTGC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTGAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGCCTGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAG TTCTGTCTCG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCG

20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGCAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTTGAG

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCACTG TGCCCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACCGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCCCTG

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAGACTT CAACCTTCA

20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACCC TTTACCTTAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 378...1799

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGATCCAAAG GACGCCCGG CGGACAGAG AATTGGTTC CGGGCCCCGG GCGATGCC	60
CCCGGTACCT CGGGCCCGTG CTCCGGTT TGTGACTGTT TCTATGTCGG AGAAGGAGGA	120
GGAGGAGGAA GAAGAAGCAA CGATTTGCTT TCTCGGTGQ TCCTCCCCCGG GCTCTACATG	180
TTCGGCCAC CGAGGAGACG GAAGAGGAGC CTGAGCCGGC CCCCGCCCGG GCGGGATT	240
TAGCTCTCG CCACAGCGGC CTCCGGCTCG CCTTGGATTC AGACCGCGAT TCGCCCGATG	300
TTTGGGAAT GGGAACTAAT GACAGCTGGC ACCCTGAACTA AGTACTTTTA TAGGCAACAC	360
CATTCCAGAA ATTCAAG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT	410
Met Asn Gly Asp Met Pro His Val Pro Ile Thr	
1 5 10	
ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CAG CTG CCT	458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro	
15 20 25	
CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT	506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Lys Ser Leu Leu Phe Asn	
30 35 40	
GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC	554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp	
45 50 55	
AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT	602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp	
60 65 70 75	
CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC	650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp	
80 85 90	
ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC	698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe	
95 100 105	
AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG	746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met	
110 115 120	
TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT	794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser	
125 130 135	
TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT	842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Arg Phe	
140 145 150 155	
GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT	890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn	
160 165 170	
AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG	938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met	
175 180 185	
CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA	986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln	
190 195 200	

GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His 205 210 215	1034
GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His 220 225 230 235	1082
GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val 240 245 250	1130
CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala 255 260 265	1178
GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly 270 275 280	1226
AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser 285 290 295	1274
CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu 300 305 310 315	1322
CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA Leu Asp Ser Pro Glu Arg Lys Gln Lys Gln Lys Met Lys Leu 320 325 330	1370
GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile 335 340 345	1418
ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser 350 355 360	1466
CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly 365 370 375	1514
GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln 380 385 390 395	1562
TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn 400 405 410	1610
CGC CCA CTA AAT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala 415 420 425	1658
TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val 430 435 440	1706
GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro 445 450 455	1754
GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr 460 465 470	1804
TCCGGAGGG AACTATGTAG TCACCCCCAG AGGCCCGACT CCTCTGGTGA GCTCTGGGCC TAGGGTGGGG GTGGTGTG TGTCTGGCG CACTGTCCC CCTACATGAT GGGTCATCC CAGTGGCTT CTCTCACCG CTTCCTCTG TGAGAGACCC TGTCAGGTG TCACTGGCTC CAGGGAGCTG TCTCTGATT CTCCAGTGA ACAGTGAGAT TTGGCACACC TCACATGAT CGCTCTGTG CTCGGAAATG TAACCATAGG TTTCTGTG TCTGGAGGA CAAGGTGAG	1864 1924 1984 2044 2104

GGCTTCCAC	TTGAGTCTCC	CTGGTGGAGC	CCAGCTCTG	ACATACCTGG	TAAAAGTTCT	2164
CAAGAAAGA	ACATGGAGGA	GGAAATGTGGA	TAACAAACCT	GGCTGCCTGT	GTGTCCTAACG	2224
CTAGGAAGAT	GTAAATGTC	CACAAACGGG	GTAATGGCT	TGCTCTGGTC	ACAGCTGTCT	2284
CAAGCCCCAG	CCCTGGGCGC	CAGCCCCAAGC	CAAAAGACTA	GGTCAGAGC	CACACAGCGC	2344
CAGGCCACAT	CCGCCTCAC	TGggACCCCT	TGTTGGGTAC	AGTCTCCGCG	CCCAACCCAGA	2404
CCTCTGAAG	GAGAGACCCC	ATGGCAAGGA	CTCAGGCCACC	TGCAAGTTCA	TAAGCCCCCA	2464
GTGGGTTCTC	ACCCCAAGCC	GGCCCTGCCT	CAGAGCAGC	ACCCAGGACG	TGCCCAGTAC	2524
GCCCCCTTC	ACCCCAAGCC	GGCCCTGCCT	CAGAGCAGC	ACCCAGGACG	TGCCCAGTAC	2584
CGGTGACTC	CACTCAATC	CTCTCTCCA	GGAGGCATGC	AAAGTGTCA	CCAGCAGGC	2644
CCCTGGAAAG	CAGTCATCAC	CTCTTAAAGG	ATTGTTGGGT	TGCGTCTCG	AACCTGCCAGG	2704
TGACGACAC	CACCCCTGTC	CGGTGTTGCA	TGACGAGGAG	CTATGACCTG	GCACAGATTC	2764
CAGCTCAAA	GGGGCACCCG	GGGGCCCCCTG	GGTCGGGGCG	GATCAGCTTT	CCCTGGGAC	2824
ATCTGGCTCA	TTCCAGATC	CAAGGGCTCA	TGTCGTTGAC	AGGGAGGGAA	GGCTCTGCC	2884
TGCCCCCTCG	TCAGCTCTGC	TGCGCAGGC	GGGGCAGCT	GGCTTTAGA	GCTGGCTCT	2944
GCCCCACTT	TCTCGTGAA	AGGAAAACAA	CTATGAGTC	GCCAAAGGCA	TCTCAAGATGC	3004
GTTTTAAAAA	ATTCTGTCG	TCCCATCTCG	CGCTCTGGG	ACTTCTCTC	3064	
TCGGTGTG	TCACCCATA	CTCTGTCACT	GGCACATTTC	CACCTGGCC	TGCCCTTGT	3124
CTCAGCTG	AACCTCTGA	AACTCTGAA	TGATTCTTA	GTTCACTGGG	GACTCGGCA	3184
GCACATCTGC	CTTCCAGATA	AAAGGGCCGC	GGGGCCCC	AGCACCTCCC	CAAGCCACAC	3244
CCCTAGCTC	CTCCCTTAC	CTCTGCAGCT	GAGGGTCTCT	TCAGGCCACCC	TTAAGTCCCC	3304
ACCTGGGCTC	CTGCCCTCCC	CTGGCTTAGC	AGCGGCCCTCT	CCACGGGGC	CCCTCTCTG	3364
CACAGAGCCC	CTCAGCTTC	CTGGGATGA	GGGGCAGGC	CATGACCTG	AAAGTCTAGC	3424
CTCTGGCTG	ACCTCCAGG	GGCCACCTCC	CCGGCCCTCTC	CCGGCCCCGG	CCCGCTCTC	3484
TGCTGCTGGC	CTCTGGTCG	TGCCCCCGAG	ACTGAGCTGC	GCTTGGGGT	CCTGGGGCC	3544
TGGGGCGTCC	CGCACCGAAC	GGAGGGCGGC	GGAAAGGGCG	GAGGTCTTC	3604	
TGGGGGCTCC	TCCGAGCTC	GAGGGCGCTG	CTTCCCCGGC	GGCGCCCCGG	TTTCTGGG	3664
AGCCCGGGCTC	TCCGCTCTCG	GGTGACCCCC	TGAGACCCCC	GGGGAGGGCC	CTTGGGAGGC	3724
GGGGGCTCTG	CTCCGGCTGC	TCACAAAGCAC	TGCGTCCCC	TCAGGAGGGA	CGCGCACCTC	3784
CACCCACGGC	GCTGGCCGCC	GCACGGCCGC	TCCTCCCGCT	CCCGCAGCCT	GGACGCCCTC	3844
CGAGGCGGCC	CCAGGCGGCC	CCACGGCGCC	CCCTCCCGCT	GGCCAGGAGC	TGCTTCCCG	3904
GAGCTGGCG	CCCCCAGGG	GGAGGAGGGC	GGCCCGAGAC	CCCTCCCGAG	CTCTCCCCAG	3964
CCACTCTGGC	CCCGCCAGCC	CCGGCTGTGTC	CGAGTGTGCG	TCTCTGGCC	GGGCTTCCC	4024
CGGGGAAGGA	AAAGCAAAAGG	CTT				4047

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear.

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

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Met Asn Gly Asp Met Pro His Val Pro Ile Thr Thr Leu Ala Gly Ile
1 5 10 15
Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro Leu Pro Ser Pro Leu
20 25 30
Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn Ala Arg Ile Ala Glu
35 40 45
Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp Asn Leu Val Ser Gln
50 55 60
Leu Val His Ser Leu Asn Gln Val Ser Thr Asp His Ile Glu Leu Lys
65 70 75 80
Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp Ile Pro Val Leu Leu
85 90 95
Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe Arg Glu Lys Ser Met
100 105 110
Gln Asn Arg Tyr Val Gln Ser Gly Met Met Ser Gln Tyr Lys Leu
115 120 125
Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln
130 135 140
Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr
145 150 155 160
Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser
165 170 175
Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro
180 185 190
Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser
195 200 205

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Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
 210 215 220
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
 225 230 235
 His Gly Ser Ser Gly Asp Tyr Leu His Met Val His Arg Leu Ser Ser
 245 250 255
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
 260 265 270
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
 275 280 285
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
 290 295 300
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
 305 310 315 320
 Arg Lys Gln Lys Lys Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
 325 330 335
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
 340 345 350
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
 355 360 365
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
 370 375 380
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
 385 390 395 400
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
 405 410 415
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
 420 425 430
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
 435 440 445
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
 450 455 460
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 26...799

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTG AATTGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG Ala Thr Gln Ala Ile Phe Glu Ile Leu	52
	1 5
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	100
	15 20 25
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	148
	30 35 40
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	196
	45 50 55
CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Gln	244
	60 65 70
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292

Gly	Leu	Gln	Met	Val	Lys	Lys	Asn	Phe	Glu	Trp	Val	Ala	Glu	Arg	Val
75					80						85				
GAG	TTG	CTT	TTG	AAA	TCA	GAA	AGT	CAG	TGC	AGG	GTT	GTA	GTG	TTG	ATG
Gl	Leu	Leu	Leu	Lys	Ser	Glu	Ser	Gln	Cys	Arg	Val	Val	Val	Leu	Met
90					95					100					105
GGC	TCT	ACT	TCT	GAT	CTT	GGT	CAC	TGT	GAA	AAA	ATC	AAG	AAG	GCC	TGT
Gly	Ser	Thr	Ser	Asp	Leu	Gly	His	Cys	Glu	Ile	Lys	Ile	Lys	Ala	Cys
110						115				120					
GGA	AAT	TTT	GGC	ATT	CCA	TGT	GAA	CTT	CGA	GTA	ACA	TCT	GCG	CAT	AAA
Gly	Asn	Phe	Gly	Ile	Pro	Cys	Glu	Leu	Arg	Val	Thr	Ser	Ala	His	Lys
125						130				135					
GGA	CCA	GAT	GAA	ACT	CTG	AGG	ATT	AAA	GCT	GAG	TAT	GAA	GGG	GAT	GGC
Gly	Pro	Asp	Glu	Thr	Leu	Arg	Ile	Lys	Ala	Glu	Tyr	Glu	Gly	Asp	Gly
140						145				150					
ATT	CCT	ACT	GTA	TTT	GTG	GCA	GTG	GCA	GCC	AGA	AGT	AAT	GGT	TTG	GGA
Ile	Pro	Thr	Val	Phe	Val	Ala	Val	Ala	Gly	Arg	Ser	Asn	Gly	Leu	Gly
155					160					165					
CCA	GTG	ATG	TCT	GGG	AAC	ACT	GCA	TAT	CCA	GTT	ATC	AGC	TGT	CCT	CCC
Pro	Val	Met	Ser	Gly	Asn	Thr	Ala	Tyr	Pro	Val	Ile	Ser	Cys	Pro	Pro
170						175				180					185
CTC	ACA	CCA	GAC	TGG	GGA	GTT	CAG	GAT	GTG	TGG	TCT	TCT	CTT	CGA	CTA
Leu	Thr	Pro	Asp	Trp	Gly	Val	Gln	Asp	Val	Trp	Ser	Ser	Leu	Arg	Leu
190						195				200					
CCC	AGT	GGT	CTT	GGC	TGT	TCA	ACC	GTA	CTT	TCT	CCA	GAA	GGG	TCA	GCT
Pro	Ser	Gly	Leu	Gly	Cys	Ser	Thr	Val	Leu	Ser	Pro	Glu	Gly	Ser	Ala
205						210				215					
CAA	TTT	GCT	GCT	CAG	ATA	TTT	GGG	TTA	AGC	AAC	CAT	TTG	GTA	TGG	AGC
Gln	Phe	Ala	Ala	Gln	Ile	Phe	Gly	Leu	Ser	Asn	His	Leu	Val	Trp	Ser
220						225				230					
AAA	CTG	CGA	GCA	AGC	ATT	TTG	AAC	ACA	TGG	ATT	TCC	TTG	AAG	CAG	GCT
Lys	Leu	Arg	Ala	Ser	Ile	Leu	Asn	Thr	Trp	Ile	Ser	Leu	Lys	Gln	Ala
235						240				245					
GAC	AAG	AAA	ATC	AGA	GAA	TGT	ATT	TTA	TAAGAAGAA	TGCCATTGAA	TTTTTTA				826
Asp	Lys	Ile	Arg	Glu	Cys	Asn	Leu								
250						255									
GGGGAAAAAC	TACAAATTTC	TAATTTAGCT	GAAGGGAAAAT	CAAGCAAGAT	GAAGGGTAA										886
TTTTAAATTA	GAGAACACAAA	ATAAAATGTA	TTAGTGAAATA	ATTGTTGAGG	GTAGGCTTAT										946
TCAGATGCAA	GGCCAGCAAT	GGGGCTCCCC	ATTATCCCCA	CCCTTTGGT	CCAGGTCCCC										1006
TTCCTGCAAA	TGGGACACCA	TAGGAGAGAG	ACAAAGGGATA	TTAGACGCAA	CATCATTTGGC										1066
CCAGGGGAGT	CGGAGAGAGA	CTGGCATATTG	CTGCAAGGGC	ATTTCAGGCG	TCTGTCTTGG										1126
GTCAGGGAGC	ACACAGCATT	GTGGAAGAGC	AGCACGCTTG	CCAGGGAGTC	TTTTTGTCAT										1186
AGCCGTTGCG	TGTGAAAGTG	ATGCCATTGG	TCCTGGGAATG	AAAGCCCTGTG	GGCAGGAGAAGA										1246
TAGACAGGGC	AGCAACTTCT	GGGGCTCTCC	GGCCCTCTTC	CACCATAGCA	ATGTTGGGCAA										1306
AACTGGTGC	AGGCCCCAAC	TAGGAGAGAG	AGCCCAAGGC	AGAGGGCAAG	TGACAAAGGA										1366
TGTACCATGT	CCAACTCTCC	ACACCCCTGG	GTGCCCCCTC	CCATATGTCCT	TCTTGTATGC										1426
CAAGTTGGC	TGGGAGCAGC	TCACTGCTCTC	TCTAGGCTAGG	AGGGTTCTTC	AGCTCTCTGG										1486
GGCCCCAGCT	TGTGTTGAA	GTGCTGCAAGG	GTGCTGCTCA	CTGTTTCTC	GTCTCCAGCA										1546
AAGTAGGGCG	ACACAGCATT	GTGGAAGAGC	AGCACGCTTG	TTGTCATCAC	CTTGATCTTG										1606
TTTTCTTCCA	GGAAACTTGTG	CTTGATGCGC	ACATCTCCCC	GCACGCTCTC	ATACTTGTC										1666
CGATGGCGCT	GGAAAGTGGC	CTGGGCACTC	TCAGTTGCG	CAAGCTGTC	TCGATCTCCG										1726
GGGCTTAGAC	TCACTCTCTC	TAAGCTGTTG	CGGTAGGCT	CATATCCAG	CTGGCAGCC										1786
TCACTATGTT	TCACAGCTAC	GAGGCTGTCT	TCCATGGCT	TGTTGACCAA	TGTGTTGATG										1846
CTAGAGACAA	AGAAGTTCAT	GGCTCTAGC	AGGGTTCTCC	ATTCTTGCA	TAGTAGTTTC										1906
TGTGTCCTG	CATTGTAAC	AAATCCCTCC	TGAACGCTTG	GGGACTCTC	GCTGAGGTC										1966
GCAGAACGCT	CACCCAGTGT	ATGCTGGGTC	TGCAAGCAGG	TGAGAGGTC	GGCTGTCAGT										2026
GGCCGGCCCA	GCTGCAAGGAC	ACTCTCTACAT	TTGCGCTTC	TCTCACCGAG	CAACTCTAAC										2086
TGCACTGCTA	GCTCCAGGAT	TCCGGCCCT	CCACTCCGTC	CCCCGGGGT	CTGCTCTGTG										2146
TGCGATGAC	GGCATATAGC	TGTTGATCA	AAAGCAGGAG	CTGACGAGCT	CTGACGAGCT										2206
TTCTCTACT	TGTGTCATCA	ACGGCAAGCT	TGTTGATCA	AAAGCAGGAG	CTTCTGAGC										2266
AAACAGGAAT	GACAGCAAGA	AGTTCAAAAGG	TGACAGCAAGA	GGTCAAGGCG	TCCTCCCTAG										2326
ATGATGCCAC	ATCCGGAAAG	TCCCCATCGA	CGTCACGGAG	GGGGAAAGTC	TCTCCCTGGG										

GCTGCCCTT	GGGAAGGTCA	CCAACCTCT	GATGCTGAAG	GGGAAAAACC	AGGCCTTCAT	2446
CGAGATGAC	ACGGAGGAGG	CTGCAAAC	CATGGTGAAC	TACTACACT	CGGTGACCC	2506
TGTGCTGCCG	GGCCAGCCCCA	TCTACATCCA	GTTCCTCCAAAC	CACAAGGAGC	TGAAGACCGA	2566
CAGCTCTCC	AACCAAGGGC	GGGCCCTGGC	GGCCGTGGAT	GCAGGGATGG	CGATGCCCG	2626
GGGGAAACCTG	GCCTTGCTG	CCTCGCCG	GGCCGTGGAT	GCAGGGATGG	CGATGCCCG	2686
GCAGAGCCCC	GTGCTCAGGA	TCTACGTGGA	GAACCTCTTC	TACCCCTGTA	CCCTGGATGT	2746
GCTGCCACAG	ATTTCCTCC	ATTCCTGGAC	AGTGTGTAAG	ATCATCACCT	TCACCAAGAA	2806
CAACCACTG	CAGGGCCCTGC	TGCAAGTATGC	GGACCCCCGTC	AGGGCCCAAGE	ACGCCAAGCT	2866
GTCGCTGGAC	GGCAGAACACA	TCTACAAACCC	CTGCTGCAAC	CTGCGCATCC	ACTTTTCAA	2926
GTCACCAAGC	CTCAACGTCA	AGTACAACAA	TGACAAAGAGC	CGTGAATAC	TCGTGCCGAA	2986
TTCTTGGAT						2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala	Thr	Gln	Ala	Ile	Phe	Glu	Ile	Leu	Glu	Ser	Trp	Leu	Pro	Gln		
1							5		10					15		
Asn	Cys	Thr	Leu	Val	Asp	Met	Lys	Ile	Glu	Phe	Gly	Val	Asp	Val	Thr	
							20		25					30		
Thr	Lys	Glu	Ile	Val	Leu	Ala	Asp	Val	Ile	Asp	Asn	Asp	Ser	Trp	Arg	
							35		40					45		
Leu	Trp	Pro	Ser	Gly	Asp	Arg	Ser	Gln	Gln	Lys	Asp	Lys	Gln	Ser	Tyr	
							50		55					60		
Arg	Asp	Leu	Lys	Glu	Val	Thr	Pro	Glu	Gly	Leu	Gln	Met	Val	Lys		
							65		70					75		80
Asn	Phe	Glu	Trp	Val	Ala	Glu	Arg	Val	Glu	Leu	Leu	Leu	Lys	Ser	Glu	
							85		90					95		
Ser	Gln	Cys	Arg	Val	Val	Val	Leu	Met	Gly	Ser	Thr	Ser	Asp	Leu	Gly	
							100		105					110		
His	Cys	Glu	Lys	Ile	Lys	Lys	Ala	Cys	Gly	Asn	Phe	Gly	Ile	Pro	Cys	
							115		120					125		
Glu	Leu	Arg	Val	Thr	Ser	Ala	His	Lys	Gly	Pro	Asp	Glu	Thr	Leu	Arg	
							130		135					140		
Ile	Lys	Ala	Glu	Tyr	Glu	Gly	Asp	Gly	Ile	Pro	Thr	Val	Phe	Val	Ala	
							145		150					155		160
Val	Ala	Gly	Arg	Ser	Asn	Gly	Leu	Gly	Pro	Val	Met	Ser	Gly	Asn	Thr	
							165		170					175		
Ala	Tyr	Pro	Val	Ile	Ser	Cys	Pro	Pro	Leu	Thr	Pro	Asp	Trp	Gly	Val	
							180		185					190		
Gln	Asp	Val	Trp	Ser	Ser	Leu	Arg	Leu	Pro	Ser	Gly	Leu	Gly	Cys	Ser	
							195		200					205		
Thr	Val	Leu	Ser	Pro	Glu	Gly	Ser	Ala	Gln	Phe	Ala	Ala	Gln	Ile	Phe	
							210		215					220		
Gly	Leu	Ser	Asn	His	Leu	Val	Trp	Ser	Lys	Leu	Arg	Ala	Ser	Ile	Leu	
							225		230					235		240
Asn	Thr	Trp	Ile	Ser	Leu	Lys	Gln	Ala	Asp	Lys	Lys	Ile	Arg	Glu	Cys	
							245		250					255		
Asn	Leu															

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile	Gln	Arg	Phe	Gly	Thr	Ser	Gly	His	Ile	Met	Asn	Leu	Gln	Ala	Gln	
1							5		10					15		

Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
 20 25 30
 Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
 35 40 45
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
 50 55 60
 Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
 65 70 75 80
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
 85 90 95
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
 100 105 110
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Val Ser Asp
 115 120 125
 Ser Ser Trp Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
 130 135 140
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
 145 150 155 160
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
 165 170 175
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
 180 185 190
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
 195 200 205
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
 210 215 220
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
 225 230 235 240
 Arg Gln Gly Pro Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
 245 250 255
 Lys Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln
 260 265 270
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
 275 280 285
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
 290 295 300
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
 305 310 315 320
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
 325 330 335
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
 340 345 350
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
 355 360 365
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
 370 375 380
 Leu Phe Leu His His Trp Pro Leu Gln Pro Pro Gly Ser Leu
 385 390 395 400
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
 405 410 415
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
 420 425 430
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
 435 440 445
 Thr Arg Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
 450 455 460
 Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
 465 470 475 480
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
 485 490 495
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
 500 505 510
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
 515 520 525
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
 530 535 540
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
 545 550 555 560
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
 565 570 575
 Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
 580 585 590
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg

595 600 605
 Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys
 610 615 620
 Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr
 625 630 635 640
 Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu
 645 650 655
 Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro
 660 665 670
 Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser
 675 680 685
 Thr Ile Pro Ala Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr
 690 695 700
 Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val
 705 710 715 720
 Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly
 725 730 735
 Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala
 740 745 750
 Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp
 755 760 765
 Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr
 770 775 780
 Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu
 785 790 795 800
 Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu
 805 810 815
 Asn Lys Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu
 820 825 830
 Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg
 835 840 845
 Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu
 850 855 860
 Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe
 865 870 875 880
 Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu
 885 890 895
 Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu
 900 905 910
 Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu
 915 920 925
 Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu
 930 935 940
 Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln
 945 950 955 960
 Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala
 965 970 975
 Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp
 980 985 990
 Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly
 995 1000 1005
 Gly Glu Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg
 1010 1015 1020
 Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Gln Lys Ala
 1025 1030 1035

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro
 1 5 10 15
 Ile Glu Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro
 20 25 30
 Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly
 35 40 45

Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
 50 55 60
 Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
 65 70 75 80
 Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
 85 90 95
 Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
 100 105 110
 Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
 115 120 125
 Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
 130 135 140
 Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
 145 150 155 160
 Tyr Phe Glu Phe Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
 165 170 175
 Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
 180 185 190
 Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
 195 200 205
 Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
 210 215 220
 Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Gly
 225 230 235 240
 Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
 245 250 255
 Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
 260 265 270
 Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
 275 280 285
 Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
 290 295 300
 Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
 305 310 315 320
 Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
 325 330 335
 Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Phe
 340 345 350
 Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
 355 360 365
 Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
 370 375 380
 His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
 385 390 395 400
 Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
 405 410 415
 Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
 420 425 430
 Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
 435 440 445
 Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
 450 455 460
 Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
 465 470 475 480
 Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
 485 490 495
 Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
 500 505 510
 Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
 515 520 525
 Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
 530 535 540
 Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
 545 550 555 560
 Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
 565 570 575
 Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
 580 585 590
 Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
 595 600 605
 Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
 610 615 620
 Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

625 630 635 640
 Val Tyr Met Ser Ile Cys Gly Glu Asn Glu Asn Cys Pro Pro Gly Val
 645 650 655 660
 Gly Ala Cys Phe Gly Gln Thr Arg Ile Ser Val Gly Lys Ala Asn Lys
 660 665 670 675
 Arg Leu Arg Tyr Val Asp Gln Val Leu Gln Leu Val Tyr Lys Asp Gly
 675 680 685 690
 Ser Pro Cys Pro Ser Lys Ser Gly Leu Ser Tyr Lys Ser Val Ile Ser
 690 695 700 705
 Phe Val Cys Arg Pro Glu Ala Gly Pro Thr Asn Arg Pro Met Leu Ile
 705 710 715 720
 Ser Leu Asp Lys Gln Thr Cys Thr Leu Phe Phe Ser Trp His Thr Pro
 725 730 735 740
 Leu Ala Cys Glu Gln Ala Thr Glu Cys Ser Val Arg Asn Gly Ser Ser
 740 745 750 755
 Ile Val Asp Leu Ser Pro Leu Ile His Arg Thr Gly Gly Tyr Glu Ala
 755 760 765 770
 Tyr Asp Glu Ser Glu Asp Asp Ala Ser Asp Thr Asn Pro Asp Phe Tyr
 770 775 780 785
 Ile Asn Ile Cys Gln Pro Leu Asn Pro Met His Gly Val Pro Cys Pro
 785 790 795 800
 Ala Gly Ala Ala Val Cys Lys Val Pro Ile Asp Gly Pro Pro Ile Asp
 805 810 815 820
 Ile Gly Arg Val Ala Gly Pro Pro Ile Leu Asn Pro Ile Ala Asn Glu
 820 825 830 835
 Ile Tyr Leu Asn Phe Glu Ser Ser Thr Pro Cys Gln Glu Phe Ser Cys
 835 840 845 850
 Lys

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
 1 5 10 15
 Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
 20 25 30 35
 Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
 35 40 45 50
 Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
 50 55 60 65
 Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys
 65 70 75 80
 His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
 85 90 95 100
 Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
 100 105 110 115
 Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
 115 120 125 130
 Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
 130 135 140 145
 Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
 145 150 155 160
 Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
 165 170 175 180
 Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
 180 185 190 195
 Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser
 195 200 205 210
 Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
 210 215 220 225
 Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
 225 230 235 240
 Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
 245 250 255

Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
 260 265 270
 Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
 275 280 285
 Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
 290 295 300
 Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Asp
 305 310 315 320
 Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
 325 330 335
 Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
 340 345 350
 His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
 355 360 365
 Arg Gln Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro
 370 375 380
 Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
 385 390 395 400
 Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
 405 410 415
 Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
 420 425 430
 Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
 435 440 445
 Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
 450 455 460
 Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
 465 470 475 480
 Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
 485 490 495
 Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
 500 505 510
 Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu His
 515 520 525
 Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
 530 535 540
 Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
 545 550 555 560
 Phe Ile Ala Arg Tyr Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
 565 570 575
 Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
 580 585 590
 Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Trp Gly Leu Ala Arg His
 595 600 605
 Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
 610 615 620
 Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
 625 630 635 640
 Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
 645 650 655
 Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
 660 665 670
 Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
 675 680 685
 Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
 690 695 700
 Lys Asp Phe Glu Val Arg His Gly Asp Glu Asp Thr Ile Lys Glu Met
 705 710 715 720
 Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
 725 730 735
 Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
 740 745 750
 Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
 755 760 765
 Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Arg Asp Gln
 770 775 780
 Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
 785 790 795 800
 Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile
 805 810 815
 Gln Leu Gly Glu Asp Glu Asp Glu Asp Glu Met Asp Asp Leu Glu Pro Asn
 820 825 830
 Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

835	840	845
Leu Lys Glu Asp		
850		

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

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Met Phe Ser Ala Leu Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
 1           5          10         15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
 20          25         30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
 35          40         45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
 50          55         60
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
 65          70         75         80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
 85          90         95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
100         105        110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala
115         120        125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
130         135        140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145         150        155         160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
165         170         175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg
180         185         190
Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg
195         200         205
Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His
210         215         220
Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu
225         230         235         240
Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu
245         250         255
Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu
260         265         270
Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala
275         280         285
Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala
290         295         300
Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala
305         310         315         320
Pro Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val
325         330         335
Pro Pro Ser Glu Ala Leu Pro Pro Ala Cys Pro Ser Ala Pro Ala
340         345         350
Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr
355         360         365
Glu Ala Ala Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro
370         375         380
Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Arg Asp Leu Asp
385         390         395         400
Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val
405         410         415
Gly Ala Lys Ala Ala Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu
420         425         430
Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu
435         440         445
Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser
450         455         460

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Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
465 470 475 480
Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
485 490 495
Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
500 505 510
Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr
515 520 525
Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
530 535 540
Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
545 550 555 560
Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
565 570 575
Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
580 585 590
Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
595 600 605
Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
610 615 620
Ser Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser
625 630 635 640
Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
645 650 655
Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
660 665 670
Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
675 680 685
Tyr Ser Glu Ser Tyr
690